

GenCore version 4.5
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OM protein - protein search, using SW model

Run on:

March 1, 2001, 16:09:13 ; Search time 299.73 Seconds

(without alignments)
17.597 Million cell updates/sec

Title: US-09-331-631A-3_COPY_29_73

Perfect score: 252

Sequence: 1 SEFDROEYECKRQCMQLET..... RCVSQCDKRFEEIDWWSKYD 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_15:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	252	100.0	666	10 Q9SP15
2	252	100.0	666	10 Q9SP14
3	180	71.4	625	10 Q9SP13
4	70.5	28.0	593	10 Q43358
5	70.5	28.0	593	10 Q9SEW4
6	67	26.6	810	10 Q9ZWI3
7	67	26.6	170	6 Q8B179
8	65	25.8	393	10 Q9ZTP0
9	64	25.4	554	10 Q9SG14
10	63	25.0	6	Q9TTS4
11	62.5	24.8	489	10 Q9SP11
12	62	24.6	875	4 Q60278
13	62	24.6	941	4 Q9UKY2
14	62	24.6	941	4 Q9UHF8
15	62	24.6	941	4 Q9HZ08
16	62	24.6	1947	2 Q9RFK7
17	61	24.2	554	10 P93719
18	61	24.2	930	11 Q9JJ23
19	59.5	23.6	5	Q9VTH3

ALIGMENTS

RESULT	1	
ID	Q9SP15	
AC	Q9SP15;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DE	VICILIN PRECURSOR.	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viriplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Proteaceae; Macadamia.	
OX	NCBI_TaxID=60698;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE-NUT KERNEL.	
RA	Marcus J.P., Goliiter K.C., Green J.L., Manners J.M.;	
RT	"A family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia kernels."	
RL	Plant J. 0-0-0(1999).	
DR	EMBL; AFI16183; RAD54244.1; -.	
DR	EMBL; P02833; 20HL.	
DR	INTERPRO; IPR001113; -.	
DR	PRAM; PR00546; Seedstore_7S; 1.	
SQ	SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64;	
Query	Match	100.0%; Score 252; DB 10; Length 666;
Best Local Similarity	100.0%; Pred. No. 5.9e-24;	
Matches	45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Conservative	0;	

DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	DE	VICILIN PRECURSOR.
GN		CGV.	
OS	Macadamia integrifolia (Macadamia nut).	THEOBROMA CACAO (Cacao).	
OC	Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; eudicots; Rosidae; eurosids II;		
OC	Malvales; Malvaceae; Theobroma.		
OX	[1] NCBI_TaxID=60598;		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=NUT KERNEL;		
RA	Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;		
RT	"A family of antimicrobial peptides is produced by processing of a 7S		
RT	globulin protein in Macadamia integrifolia.";		
RL	Plant J. 0:0-0(1999);		
DR	EMBL: AF161884; AAD54245; 1; -.		
DR	HSSP: P02853; 2PHL.		
DR	INTERPRO: IPR001113; -.		
DR	PFAM: PF00546; Seedsstore_7s; 1.		
SQ	SEQUENCE 666 AA; 78243 MW; 0ECA22FB710F8A7B CRC64;		
Query Match	100.0%; Score 252; DB 10; Length 666;		
Best Local Similarity	100.0%; Pred. No. 5.9e-24;		
Matches	45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 SEFDQEQEYCKRQCMOLETSQGMRCVSGQCDKREEDIDWSKYD 45		
Db	29 SEFDQEQEYCKRQCMOLETSQGMRCVSGQCDKREEDIDWSKYD 73		
RESULT	3		
ID	Q9SPJ3	PRELIMINARY;	PRT; 625 AA.
AC	Q9SPJ3		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DE	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	VICILIN PRECURSOR (FRAGMENT).		
GN			
OS	Macadamia integrifolia (Macadamia nut).		
OC	Bukaryota; Viridiplantae; Embryophyta; Tracheophyta;		
OC	Magnoliophyta; eudicots; Proteaceae; Macadamia.		
OX	[1] NCBI_TaxID=60598;		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=NUT KERNEL;		
RA	Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;		
RT	"A family of antimicrobial peptides is produced by processing of a 7S		
RT	globulin protein in Macadamia integrifolia.";		
RL	Plant J. 0:0-0(1999);		
DR	EMBL: AF161883; AAD54246; 1; -.		
DR	HSSP; P02853; 2PHL.		
DR	INTERPRO; IPR001113; -.		
DR	PFAM: PF00546; Seedsstore_7s; 1.		
SQ	SEQUENCE 625 AA; 73586 MW; 415808AB9D370296 CRC64;		
Query Match	71.4%; Score 180; DB 10; Length 625;		
Best Local Similarity	100.0%; Pred. No. 6.8e-15;		
Matches	32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	14 QCMOLETSQGMRCVSGQCDKREEDIDWSKYD 45		
Db	1 QCMOLETSQGMRCVSGQCDKREEDIDWSKYD 32		
RESULT	4		
ID	Q43358	PRELIMINARY;	PRT; 525 AA.
ID	Q33358		
AC	Q33358;		
DT	01-NOV-1996 (TREMBLrel. 01, created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
Query Match	28.0%; Score 70.5; DB 10; Length 593;		
Best Local Similarity	29.4%; Pred. No. 0.44;		
Matches	10; Conservative 15; Mismatches 8; Indels 1; Gaps 1;		
QY	5 RQEYECCKRQCMOLETSQGMRCVSGQCDKREEDIDWSKYD 37		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LEAVES;		
RX	MRDLINE=92288309; PubMed=1600151;		
RA	McHenry L., Fritz P.J.;		
RT	Comparison of the structure and nucleotide sequences of vicilin genes		
RT	of cacao and cotton raise questions about vicilin evolution.;"		
RL	Plant Mol. Biol. 18:1173-1176(1992).		
DR	EMBL; X62625; CA44493.1; -.		
DR	EMBL; X62626; CA44494.1; -.		
DR	HSSP; P02853; 2PHL.		
DR	INTERPRO; IPR001113; -.		
DR	PFAM; PF00546; Seedsstore_7s; 1.		
KW	PRODOM; PD081059; -; 1.		
FT	SIGNAL 1 24 POTENTIAL.		
FT	CHAIN 25 525 AA; 60798 MW; 1914CD5C248905D CRC64;		
SQ	SEQUENCE 525 AA; 60798 MW; 1914CD5C248905D CRC64;		
Query Match	28.0%; Score 70.5; DB 10; Length 525;		
Best Local Similarity	32.4%; Pred. No. 0.39;		
Matches	11; Conservative 11; Mismatches 11; Indels 1; Gaps 1;		
QY	5 RQEYECCKRQCMOLETSQGMRCVSGQCDKREEDIDWSKYD 37		
Db	39 RQEYECCKRQCMOLETSQGMRCVSGQCDKREEDIDWSKYD 72		
RESULT	5		
ID	Q9SEW4	PRELIMINARY;	PRT; 593 AA.
AC	Q9SEW4		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DE	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).		
OS			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;		
OC	Magnoliophyta; eudicots; Juglans regia (English walnut).		
OC	Juglans regia (English walnut).		
OC	Fagales; Juglandaceae; Juglans.		
OC	NCBI_TaxID=51240;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV; SUNLAND; TISSUE=SOMATIC EMBRYO LINE:		
RA	Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;		
RT	"Identification and cloning of a cDNA encoding a vicilin-like food		
RT	Jug r 2, from English walnut kernel (Juglans regia): a major food		
RT	allergen.;"		
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF06055; AAF18269.1; -.		
DR	HSSP; P02853; 2PHL.		
DR	INTERPRO; IPR001113; -.		
DR	PFAM; PF00546; Seedsstore_7s; 1.		
FT	NON_TER 1 1		
SQ	SEQUENCE 593 AA; 69990 MW; 9BA127E19B18C008 CRC64;		

RESULT	6
Q9ZWT3	PRELIMINARY; PRT; 810 AA.
ID	092W13
AC	092W13;
DT	01-MAY-1999 (TREMBLrel. 10, last sequence update)
RT	01-MAY-1999 (TREMBLrel. 10, last sequence update)
DR	01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE	PV100.
OS	Cucurbita maxima (Pumpkin) (Winter squash).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Cucurbitales; Cucurbitaceae; Cucurbita.
OC	OC
OX	NCBT_TaxID=3661;
RN	SEQUENCE FROM N.A.
RC	STRAIN=KUROKAWA_AMAKURI_NANKIN; TISSUE=COTYLEDON;
RX	MEDLINE=9307919; PubMed=9891029;
RA	Yamada K., Shinoda T., Kondo M., Nishimura M., Hara-Nishimura T.;
RT	"Multiple functional proteins are produced by cleaving Asn-Gln bonds of a single precursor by vacuolar processing enzyme.";
RT	J. Biol. Chem. 274:25637-25701(1999).
RL	EMBL: AB019195; BAM34056.1; .
DR	HSSP: P02653; 2PBL.
DR	INTERPRO: IPR001113; .
DR	PFAM: PF00546; Seedstore_7s; 1.
DR	PRODOM: PDO81039; -; 1.
DR	SEQUENCE 810 AA; 97314 MW; A829A3F7542266AB CRC64;
QY	5 RQEYEECKRQCMQLETS-GQMRCRVCQSQCDKRF-----EDID 40
DB	75 RAEYEVCRURQVQAERGVQKCEQVCEERLRREREQGRGEDVD 118
RESULT	7
Q28179	PRELIMINARY; PRT; 1170 AA.
AC	028179;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1998 (TREMBLrel. 08, last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE	THROMBOSPONDIN 1.
GN	TSP-1.
OS	Bos taurus (Bovine).
OC	Bukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=HOLSTEIN; TISSUE=ANTERIOR TOOTH;
RX	MEDLINE=98173773; PubMed=9507054;
RA	Inoue H.;
RT	odontoblasts and predentin";
RT	Biophys. Acta 1382:17-22(1998).
[2]	SEQUENCE OF 1-18 FROM N.A.
RC	TISSUE=AORTIC ENDOTHELIUM;
RC	Zafar R.S., Molli Y.D., Womack J.F., Walz D.A.;
RC	Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
DR	EMBL: AB005287; BAA2115.1; .
DR	EMBL: X8719; CAA60951.1; .
DR	HSSP: P3555; 1EMN.
INTERPRO	IPR000561; .
RN	[1]
RESULT	8
Q9ZTP0	PRELIMINARY; PRT; 393 AA.
ID	092ZTP0
AC	092ZTP0;
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE	HYPOTHETICAL 45.3 kDa PROTEIN.
GN	GSE705.
OS	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
OC	OC
OX	NCBI_TaxID=4530;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=LOMELLO;
RC	Subramanian P.W., Chen L.J.;
RA	Chen P.W., Chen L.J.;
RL	Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL: AF009348; NAD02494.1; .
KW	Hypothetical protein.
SQ	SEQUENCE 393 AA; 45258 MW; DBD01934BA2F9E95 CRC64;
QY	5 RQEYEECKRQCM---QLETS-GQMRCRVCQSQCDKRF-----EDID 40
DB	37 KEELRKVKKQCRWEAQDQNLRECEQICQDQEDD 74
RESULT	9
Q9SG14	PRELIMINARY; PRT; 554 AA.
ID	09SG14
AC	09SG14;
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 13, Last annotation update)
DE	PUTATIVE GTPASE ACTIVATOR PROTEIN OF RAB-LIKE SMALL GTPASES (GTPASE ACTIVATING-LIKE PROTEIN).
DE	T1G12.5 OR F2K15.210.
GN	Arabidopsis thaliana (Mouse-ear cress).
OS	Eukaryota; Viridiplantae; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC	OC
OX	NCBI_TaxID=3702;
RN	[1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome 1 BAC TIG12 genomic sequence.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
 RA Mewes H.W., Lemcke K., Mayer K.F.X., Quertermont F., Salanoubat M.,
 RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JAN 2000) to the EMBL/GenBank/DDBJ databases.
 EMBL: AC012329; AAF16581; 1;
 DR EMBL: AL122956; CAB64141; -.
 DR INTERPRO: IPR000195; -.
 DR PFAM: PF00566; TBC; 1;
 SQ SEQUENCE 554 AA; 63583 MW; 430BE1FC1D8901C CRC64;

Query Match 25.4%; Score 64; DB 10; Length 554;
 Best Local Similarity 28.2%; Pred. No. 2.7; Mismatches 18; Indels 0; Gaps 0;
 Matches 11; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 5 RQEYERCKROCMOLENSGQMRCVSOCDKRFEEIDWSK 43
 DR 148 RKEYERLRRKROKHNNGTRKLNGSETIODEDWPR 186

RESULT 10
 ID 09TRS4 PRELIMINARY; PRT; 564 AA.
 AC 09TRS4; 1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-JUN-2000 (TREMBLrel. 13, last sequence update)
 DE SCO-SPONDIN (FRAGMENT).
 OS Bos taurus (Bovine)
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SUBCOMMISSURAL ORGAN;
 RA Gobron S., Creveaux T., Monnerie H., El Bitar F., Didier R.,
 RA Herbert A., Meiniel R., Baudad M., Dastugue B., Meiniel A.;
 RT "Characterization of cattle SCO-spordin glycoprotein.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
 EMBL: AJ12107; CAB33760 1; -.
 DR INTERPRO: IPR001846; -.
 DR IPR002919; -.
 DR PFAM: PF00094; wvd; 1;
 DR PFAM: PF01826; TIL; 2.
 FT NON_TER 1
 FT NON_TER 564 564
 SQ SEQUENCE 564 AA; 60337 MW; 2E22D4242P9BBZC CRC64;

Query Match 25.0%; Score 63; DB 6; Length 564;
 Best Local Similarity 38.7%; Pred. No. 3.7; Mismatches 6; Indels 4; Gaps 1;
 Matches 12; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

QY 6 OEVYERCKROCMOLENSGQMRCVSOCD 32
 DR 480 QEVYORCAPACDRNCGEPEDCGELDNCVAGCN 510

09SP11 ID 09SP11 PRELIMINARY; PRT; 489 AA.
 AC 09SP11; 1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE SUCROSE BINDING PROTEIN HOMOLOG S-64.
 OX GN SBP.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pedra J.H.F., Delu-Filho N., Pirovani C.P., Contim L.S., Dewey R.E.,
 RA Ottoni W.C., Fontes E.P.B.;
 RT "Antisense and sense expression of a sucrose binding protein homologue
 gene from soybean in transgenic tobacco affects plant growth and
 carbohydrate partitioning in leaves.";
 RL Plant Sci. 0:0 (1999).
 DR EMBL: AF191299; AAC05723 1; -.
 DR HSSP; P02053; 2PBL.
 DR INTERPRO: IPR001113; -.
 DR PFAM: PF00546; Seedstore_7s; 1; 9BBC0D45BDECECD2 CRC64;
 SQ SEQUENCE 489 AA; 55834 MW; 9BBC0D45BDECECD2 CRC64;

Query Match 24.8%; Score 62.5; DB 10; Length 489;
 Best Local Similarity 36.6%; Pred. No. 3.7; Mismatches 15; Conservative 3; Mismatches 14; Indels 9; Gaps 2;
 Matches 15; Conservative 3; Mismatches 14; Indels 9; Gaps 2;

QY 7 RYEYERCKROCMOLE-TSGQMRCVSOCD---KRFEED 38
 DR 38 ELVTCKHQCQQRQYTESDKRTCLQQCDSMKQERKQVEE 78

RESULT 12
 ID 060278 PRELIMINARY; PRT; 875 AA.
 AC 060278; 1
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE KIA0525 PROTEIN (FRAGMENT).
 RN KIA0525.
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Primates; Catarhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
 RA Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998)
 DR EMBL: AB011097; BAA75451 1; -.
 DR MEROPS; M01.018; -.
 DR INTERPRO; IPR00130; -.
 DR INTERPRO; IPR001930; -.
 DR PFAM; PF01433; Peptidase_M1; 1.
 DR PRINTS; PR00756; ALADIPPROTE.
 DR PROSITE; PS00142; ZINC_PROTEASE;
 FT NON_TER 1
 SQ SEQUENCE 875 AA; 99522 MW; C31A77DE516DEAFE CRC64;

Query Match 24.6%; Score 62; DB 4; Length 875;
 Best Local Similarity 37.8%; Pred. No. 7.6; Mismatches 1; Indels 1; Gaps 1;

RESULT 11

Matches	14;	Conservative	4;	Mismatches	19;	Indels	0;	Gaps	0;
QY	5	ROYECKRQCMOLETSQMRRCVSQCDKRFEDIDW	41						
Db	812	RTRLEEVKGFFSSLKENGSQLRCVQQTIEENIGW	848						
RESULT	13								
Q9UKY2		PRELIMINARY;		PRT;	941 AA.				
ID	Q9UKY2								
AC	Q9UKY2;								
DR	01-MAY-2000	(TREMBLrel. 13, Created)							
DT	01-JUN-2000	(TREMBLrel. 14, Last annotation update)							
DE	ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE.								
OS	Homo sapiens (Human);								
OC	Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartochini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RP									
SEQUENCE FROM N.A.									
RA	MEDLINE:99238715; PubMed=10220586;								
RA	Hattori A., Matsumoto H., Mizutani S., Tsujimoto M.; "Molecular cloning of adipocyte-derived leucine aminopeptidase highly related to placental leucine aminopeptidase/oxytocinase."; J. Biochem. 125:931-938(1999).								
RL	EMBL; AF106037; AAF07395.1; -.								
DR	INTERPRO; IPR000130; -.								
DR	INTERPRO; IPR001930; -.								
PFAM; PF01433; Peptidase_M1; 1.									
PRINTS; PR00756; ALADIPPTASE.									
DR	PS00142; ZINC_PROTEASE; UNKNOWN_1.								
KW	Aminopeptidase.								
SQ	SEQUENCE 941 AA; 107187 MW; 46BBER97CF78DEBC1 CRC64;								
RESULT	14								
Q9UHF8		PRELIMINARY;		PRT;	941 AA.				
ID	Q9UHF8								
AC	Q9UHF8;								
DT	01-MAY-2000	(TREMBLrel. 13, Created)							
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)							
DE	AMINOPEPTIDASE PILS.								
GN	APPLS.								
OS	Homo sapiens (Human);								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartochini; Hominidae; Homo.								
NCBI_TaxID=9606;									
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Schomburg L.; "Molecular characterization of human aminopeptidase PILS."; Submitted (Sep-1999) to the EMBL/GenBank/DDBJ databases.								
RL	EMBL; AF183569; AAF20384.1; -.								
DR	INTERPRO; IPR000130; -.								
DR	INTERPRO; IPR001930; -.								
PFAM; PF01433; Peptidase_M1; 1.									
PRINTS; PR00756; ALADIPPTASE.									
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.								
KW	Aminopeptidase.								
SQ	SEQUENCE 941 AA; 107420 MW; 2EC671FBACBF74 CRC64;								

Query Match 24.6%; Score 62; DB 4; Length 941; Best Local Similarity 37.8%; Pred. No. 8.1; Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYECKRQCMOLETSQMRRCVSQCDKRFEDIDW 41

Db 885 RTRLEEVKGFFSSLKENGSQLRCVQQTIEENIGW 921

Query Match 24.6%; Score 62; DB 4; Length 941; Best Local Similarity 37.8%; Pred. No. 8.1; Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYECKRQCMOLETSQMRRCVSQCDKRFEDIDW 41

Db 885 RTRLEEVKGFFSSLKENGSQLRCVQQTIEENIGW 921

Search completed: March 1, 2001, 16:09:13

Job time: 1557 sec

